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GenCore version 4.5
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OM protein - protein search, using sw model

October 21, 2001, 23:16:59 ; Search time 51.66 Seconds (without alignments) 1928.092 Million cell updates/sec Run on:

US-09-515-806-2

Perfect score:

1 MAGGRGAPGRGADEPPESYP.......INIKVEKKVSVLFLYSYRDD 1643 Sequence:

**BLOSUM62** Scoring table:

Gapop 10.0 , Gapext 0.5

412676 segs, 60623988 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database :

A\_Geneseq\_0601:\*

/SIDSI/gcgdata/geneseq/geneseqp/AA1980.DAT:\*
/SIDSI/gcgdata/geneseq/geneseqp/AA1981.DAT:\*
/SIDSI/gcgdata/geneseq/geneseqp/AA1982.DAT:\*
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/ SIDSI/gogdata/geneseq/geneseqp/AA1991.DAT:
/ SIDSI/gogdata/geneseq/geneseqp/AA1992.DAT:
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/SIDS1/gcgdata/geneseq/geneseqp/AA2000.DAT:\*/SIDS1/gcgdata/geneseq/geneseqp/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Novel protein kina	COsse repres negligh	Human ORFX ORF2525	Human ORFX ORF2786	Dancheatic outsaruc	Pancreatic ankaryo	Dancreatic entaruc	Rabbit err-2 alpha	Hapm-redulated enk	Novel protein kina	Human PKR protein.
		ID	AAB65663	AAB43581	AAB42761	AAB43022	AAY30046	AAY30048	AAY30047	AAR44008	AAR49849	AAB65664	AAW36139
		DB	22	21	21	21	20	20	20	14	15	22	18
		Match Length DB	1649	604	619	135	1108	1068	1115	626	626	630	550
dР	Query	Match	100.0	35.2	34.6	7.3	6.5	0.9	6.0	5.6	5.6	5.5	4.9
		Score	8511	2996	2946	623	549.5	511.5	511.5	473.5	473.5	471.5	415.5
	Result	No.	П	7	m	4	Ŋ	9	7	8	თ	10	11

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AAR82663 AAW12705 AAW25223 AAY94280 AAW2522 AAX21854 AAW77941 AAY70100 AAY85175	AAR40974 AAY70101 AAY70101 AAY85169 AAY70098 AAY70099 AAY30937 AAY22202 AAAB65611 AAM48895	AAY88707 AAY88172 AAX8172 AAX85168 AAX96770 AAX96776 AAX43320 AAX42109 AAM73533 AAB01218 AAX59566 AAX59566 AAX59148 AAX59148
16 18 18 21 18 21 21 21 21	14 21 21 21 20 20 12 13	19 21 22 20 20 21 21 21
551 551 551 551 508 371 508 651 772	690 690 705 661 711 642 733 733 745	, 447 440 440 440 440 440 440 440 440 440
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113 114 116 118 118 118	3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	

## ALIGNMENTS

AAB65663 standard; Protein; 1649 AA. AAB65663; RESULT AAB65663 

(first entry)

27-MAR-2001

Novel protein kinase, SEQ ID NO: 191.

Human; mouse; protein kinase; antiarthritic; antisclerotic; osteopathic; immunosuppressive; cardiant; renal; antiinflammatory; antiasthmatic; dermatological; antidiabetic; antiinfertility; gene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis.

Homo sapiens

WO200073469-A2

26-MAY-2000; 2000WO-US14842.

potential reported

99US-0136503 28-MAY-1999;

(SUGE-) SUGEN INC.

Plowman GD, Martinez R, Whyte D, Sudersanam S;

WPI; 2001-032161/04. N-PSDB; AAF44691.

Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease. neurodegenerative diseases and/or cancers

Claim 10; Fig 1; 310pp; English.

The present sequence is a novel protein kinase. The novel protein kinases and the nucleic acids that encode them may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune-related diseases and disorders, cardiovascular disease, neurodegenerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies expression and activity. Diseases related to down regulate kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, oxidative-stress related disorders, chronic inflammatory bowel disease, exidence of the contraction or t chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, rhinitis, autoimmunity, diabetes, cancers and reproductive disorders.

1649 AA; Sequence

Query Match

Length 1649;

ö RRKEEIKEEKKRKEMAKQERLEIASLSNQDHTSKKDPGGHRTAAILHGGSPDFVGNGKHR 240 240 VMIFELAYHVQSFLSEHNKPPPKSFHEEMLERRAQEEQQRLLEAKRKEEQEQREILHEIQ 180 PQGLTGEEVYVKVDLRVKCPPTYPDVVPEIELKNAKGLSNESVNLLKSRLEELAKKHCGE 120 Gaps 9 09 .; 0 0; Indels 100.0%; Score 8511; DB 22; 0; Mismatches Best\_Local Similarity 100. Matches 1643; Conservative 181 61 121 181

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VQLCTPLLLPRNRQIYEHNEAALFMDHSGMLVMLPFDLRIPFARYVARNNILNLKRYCIE 1140 ISAAVLNMEESVTISSCDLLVVSVGQMSMSRAINLTQKLWTAGITAEIMYDWSQSQEELQ 1440 EYCRHHEITYVALVSDKEGSHVKVKSFEKERQTEKRVLETELVDHVLQKLRTKVTDERNG 1500 REASDNLAVQNLKGSFSNASGLFEIHGATVVPIVSVLAPEKLSASTRRRYETQVQTRLQT 1560 1021 NVDGKAYRTMMAQIFSQRISPAIDYTYDSDILKGNFSIRTAKMQQHVCETIIRIFKRHGA 1080 RVFRPRKLDRFHPKELLECAFDIVTSTTNSFLPTAEIIYTIYEIIQEFPALQERNYSIYL 1200 NHTMLLKAILLHCGIPEDKLSQVYIILYDAVTEKLTRREVEAKFCNLSLSSNSLCRLYKF 1260 961 KFPEDFDDGEHAKQKSVISWLLNHDPAKRPTATELLKSELLPPPQMEESELHEVLHHTLT 1020 MVGTALYVSPEVQGSTKSAYNQKVDLFSLGIIFFEMSYHPMVTASERIFVLNQLRDPTSP 960 780 900 1561 SLANLHQKSSEIEILAVDLPKETILQFLSLEWDADEQAFNTTVKQLLSRLPKQRYLKLVC fgavikvgnkldgccyavkripinpasrqfrrikgevtllsrlhhenivryynawierhe NGCHESEPSVTTEAVHYLYIQMEYCEKSTLRDTIDQGLYRDTVRLWRLFREILDGLAYIH EKGMIHRDLKPVNIFLDSDDHVKIGDFGLATDHLAFSADSKQDDQTGDLIKSDPSGHLTG ARFPATGPGSSDDEDDDEDEHGGVFSQSFLPASDSESDIIFDNEDENSKSQNQDEDCNEK 1621 DEIYNIKVEKKVSVLFLYSYRDD 1643 1621 deiynikvekkvsvlflysyrdd 1643 1381 1441 1501 901 1081 1201 781 1201 601 721 qq qq g g g δy qq δλ q qq QΥ δ οy Qγ Q δ qq Óγ qq Qγ q δy q Qλ QQ δ дq ŏ pp ÓΥ qq óγ Qγ

AAB43581 RESULT

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Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antirheumatic; antiarthritic; antidiral; antintlammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; cagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
                                                               Human cancer associated protein sequence SEQ ID NO:1026.
AAB43581 standard; Protein; 604 AA.
                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                   08-MAR-2000; 2000WO-US05882
                                         08-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                Rosen CA, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-587533/55.
                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAC77790.
                                                                                                                                                                                                                         WO200055350-A1.
                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                       12-MAR-1999;
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99US-0124270

ANALYON, to AALV848 encode the numan cancer associated protents given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities concluded include cytostatic; proliferative; vulnerary; immunomodulator; antidabetic; antiasthmatic; antihaleratic; antibacterial; antiviral; antiinflammatory; antithyroid; antihaleratic; antibacterial; antiviral; concluding antidaleratic; antibacterial; antiviral; concluding and polypeptides can be used for preventing, treating or polynucleotides and polypeptides and biggnosing pathological conditions. Polynucleotides, polypeptides and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoists and organ correction, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, and infections, and isorders, neurological disease and cancers and antagonists may be also be used in drug screens. AAC78449 to the present sequences used in the exemplification of the present invention or also be used in the exemplification of the present invention. The periods in the exemplification of the present invention or also be used in the exemplification of the present invention. AAC77607 to AAC78448 encode the human cancer associated proteins given Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer -Claim 11; Page 1609-1611; 2352pp; English. the present invention.

604 AA; Sequence

ö 0; Gaps 35.2%; Score 2996; DB 21; Length 604; 99.7%; Pred. No. 2e-239; Live 0; Mismatches 2; Indels 0; 2; Indels Query Match 35.2 Best Local Similarity 99.7 Matches 593; Conservative

1049 SDILKGNFSIRTAKMQQHVCETIIRIFKRHGAVQLCTPLLLPRNRQIYEHNEAALFMDHS 1108 

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GMLVMLPFDLRIPFARYVARNNILNLKRYCIERVFRPRKLDRFHPKELLECAFDIVTSTT 1168
                                                                  NSFLPTAEIIYTIYEIIQEFPALQERNYSIYLNHTMLLKAILLHCGIPEDKLSQVYIILY 1228
                                                                                                                               1229 DAVTEKLTRREVEAKFCNLSLSSNSLCRLYKFIEQKGDLQDLMPTINSLIKQKTGIAQLV 1288
                                                                                                                                                                                                1289 KYGLKDLBEVVGLLKKLGIKLQVLINLGLVYKVQQHNGIIFQFVAFIKRRQRAVPEILAA 1348
                                                                                                                                                                                                                                                                1349 GGRYDLLIPQFRGPQALGPVPTAIGVSIAIDKISAAVLNMEESVTISSCDLLVVSVGQMS 1408
                                                                                                                                                                                                                                                                                                                                 1409 MSRAINLTQKLWTAGITAEIMYDWSQSQEELQEYCRHHEITYVALVSDKEGSHVKVKSFE 1468
                                                                                                                                                                                                                                                                                                                                                                                                 1469 KERQTEKRVLETELVDHVLQKLRTKVTDERNGREASDNLAVQNLKGSFSNASGLFEIHGA 1528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1529 TVVPIVSVLAPEKLSASTRRRYETQVQTRLQTSLANLHQKSSEIEILAVDLPKETILQFL 1588
               483
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                                                                                                                                                1589 SLEWDADEQAFNTTVKQLLSRLPKQRYLKLVCDEIYNIKVEKKVSVLFLYSYRDD 1643
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Human ORFX ORF2525 polypeptide sequence SEQ ID NO:5050. AAB42761 standard; Protein; 619 AA. 08-FEB-2001 (first entry) AAB42761; AAB42761

W Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
W vulnerary; antipaciatic; antiparkinsonian; nootropic; neuroprotective;
W vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
W inmunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
W pypotensive; dermatological; immunosuppressive; antidiabetic;
W antiviral; antibacterial; antifungal; antitheumatic; antidiapetic;
W antiviral; antibacterial; antifungal; antitheumatic; antidyroid;
antiviral; antibacterial; antifungal; safet vs host disease;
W neurodegenerative disorder; proliferative disorder; hypertension;
N cardiovascular disease; diabetes mellitus; hypothyroidsm; SCID; ALDS;
Cholesterol ester storage; systemic lupus erythematosus; infection;
Severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
M allergy; aplastic annaemia; nocturnal heemoglobinuria; burn; wound;
W bone damage; cartilage damage; antiinfiammatory disease; coagulation;
W thrombosis; contraceptive.

Homo sapiens.

WO200058473-A2.

05-0CT-2000

31-MAR-2000; 2000WO-US08621

99US-0127636 99US-0127607 31-MAR-1999; 02-APR-1999; 

ij 1214 GIPEDKLSQVYIILYDAVTEKLTRREVEAKFCNLSLSSNSLCRLYKFIEQKGDL--QDLM 1271 1272 PTINSLIKQKTGIAQLVKYGLKDLEEVVGLLKKLGIKLQVLINLGLVYKVQQHNGIIFQF 1331 1332 VAFIKRRQRAVPEILAAGGRYDLLIPQFRGPQALGPVPTAIGVSIAIDKISAAVLNMEES 1391 1392 VTISSCDLLVVSVGQMSMSRAINLTQKLWTAGITAEIMYDWSQSQEELQEYCRHHEITYV 1451 1034 IFSQRISPAIDYTYDSDILKGNFSIRTAKMQQHVCETIIRIFKRHGAVQLCTPLLLPRNR 1093 1094 QIYEHNEAALFWDHSGMLVMLPFDLRIPFARYVARNNILNLKRYCIERVFRPRKLDRFHP 1153 1154 KELLECAFDIVTSTTNSFLPTAEIIYTIYEIIQEFPALQERNYSIYLNHTMLLKAILLHC 1213 242 nnxnslikqktgiaqlvkyglkdleevvgllkklgiklqvlinlglvykvqqhnglifqf 301 Gaps 2 ifsqrispsidytydsdilkgnfsirtakmqqhvcetiirifkrhgavqlctplllprnr 61 2; 34.6%; Score 2946; DB 21; Length 619; 95.8%; Pred. No. 2.9e-235; tive 9; Mismatches 15; Indels 2 al Similarity 95.8 586; Conservative Query Match Best Local S Matches ద ò g οy

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1452 ALVSDKEGSHVKVKSFEKERQTEKRVLETELVDHVLQKLRTKVTDERNGREASDNLAVQN 1511
                                                                                                                 1512 LKGSFSNASGLFEIHGATVVPIVSVLAPEKLSASTRRRYETQVQTRLQTSLANLHQKSSE 1571
                                                                                                                                                                                                                             1572 IEILAVDLPKETILQFLSLEWDADEQAFNTTVKQLLSRLPKQRYLKLVCDEIYNIKVEKK 1631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bone damage; cartilage damage; antiinflammatory disease; coagulation;
                             open reading frame; ORFX; detection; cytostatic; hepatotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ORFX ORF2786 polypeptide sequence SEQ ID NO:5572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 4757-4758; 5507pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB43022 standard; Protein; 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-APR-1999; 990S-0127636.
05-APR-1999; 990S-0127728.
30-MAR-2000; 2000US-0540763.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                        1632 VSVLFLYSYRDD 1643
                                                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
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02-APR-1999;
05-APR-1999;
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WPI; 1999-469338/39. N-PSDB; AAX86563.

Shi Y;

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immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antificammatory; antibacterial; antiviral; antifungal; antirhemmatic; antithyzoid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus bacterial or fungal infection, malaria, autoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pancreatic eukaryotic translation initiation factor-2 alpha kinase; PEK; eukaryotic translation initiation factor-2 alpha; pancreatic islet; drug discovery; drug development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           981 LLNHDPAKRPTATELLKSELLPPPQMEESELHEVLHHTLTNVDGKAYRTMMAQIFSQRIS 1040
                                                                                                                                                                                                                                                                                                                                                                                                          921 NOKVDLFSLGIIFFEMSYHPMVTASERIFVLNQLRDPTSPKFPEDFDDGEHAKQKSVISW 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pancreatic eukaryotic translation initiation factor-2 alpha kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "hydrophobic region; potential transmembrane
                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                             Score 623; DB 21; Length 135;
Pred. No. 1e-43;
2; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "consensus N-myristylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "consensus N-myristylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           region
                                                                                                                                                                                                                                                                                                                                        7.3%;
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                                                                                                                                                                                                                                                                                                                                                                           Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .532
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                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                          135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 initiation factor-2 alpha kinase (PEK). PEK phosphorylates eukaryotic translation initiation factor-2 alpha. PEK polynucleotides was cloned from pancreatic islet DNA libraries. The PEK nucleic acids and protein can be used as tools for drug discovery and development.
                                                                                                                                                                                                                                                                                                                                                                                                                             584 SRYFIEFEELQLLGKGAFGAVIKVQNKLDGCCYAVKRIPINPASRQFRRIKGEVTLLSRL 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                  644 HHENIVRYYNAWIERHERPAGPGTPP-------PDSGPLAKDDRAARG 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          639 ehpgivryfnawle-----tppekwqeemdeiwlkdestdwplsspsmdapsvki 689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 750 ahnlqdscltdcdmedgtvdgddeghsfelcpseaspytrsregtsssivfedsgcdnas 809
                                                                                                                                                                                    The present sequence represents a pancreatic eukaryotic translation
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                                                                                        Novel rat and human pancreatic eukaryotic translation initiation factor Zalpha kinase useful for drug discovery and development
                                                                                                                                                                                                                                                                                                                                                    Query Match 6.5%; Score 549.5; DB 20; Length 1108; Best Local Similarity 29.3%; Pred. No. 4.7e-36; Matches 150; Conservative 82; Mismatches 159; Indels 121;
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                                                                                                                                            Claim 7; Page 46-50; 77pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DDED----EHGGVFSQSFLPASD-----SESDIIFDN---EDENSKS 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           771 QNQDEDCNEKNGC-----TESEPSV-------TTEAVH---- 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LKPVNIFLDSDDHVKIGDFGLATDHLAFSADSKQDDQTGDLIKSDPS-GHLTGMVGTALY 907
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                                                                                                                                                                                                                                                                                                               6.0%; Score 511.5; DB 20; Length 1068;
29.9%; Pred. No. 6.2e-33;
tive 82; Mismatches 156; Indels 121; Gaps
                                                                                                                                                                                                                                                                                                                                                                                           644 HHENIVRYYNAWIE-------RHERPAGP-GTPPPDSGPLAKDDRAARGQPA 687
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                                                                                98US-0109992.
98US-0073031.
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         Homo sapiens
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                                                                                                                                                                                                              Pancreatic eukaryotic translation initiation factor-2 alpha kinase; eukaryotic translation initiation factor-2 alpha; pancreatic islet; drug discovery; drug development.
                                                                                                                                                       Pancreatic eukaryotic translation initiation factor-2 alpha kinase.
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AAY30047 standard; Protein; 1115 AA.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                          639 LLSRLHHENIVRYYNAWIER-HERPAGPGTP--PPDSGPLA--KDDRAARGQPASDTDGL 693
                                                       694 DSVEAAAPPPILSSSVEWSTSGERSASARFPA-----TGPGSSDDEDDDDEDEHGGVFSQ 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The haem-regulated eukaryotic initiation factor 2 alpha kinase (HRI) is a potent inhibitor of protein synthesis and may have a role in the regulation of cell division. It can be used to inhibit infection and as an antiproliferative agent in cancers such as chronic myelogenous leukaemia and psoriasis. The cDNA encoding HRI can be inserted into cells to manipulate proliferation
                                                                                                                 748 SFLPASDSESDIIFDNEDENSKSQNQDEDCNEKNGCHESEPSVTTEAVHY---LYIQMEYC
                                                                                                                                                                        806 EKS-----TLRDTIDQGL--YRDTVRLWRLFREILDGLAYIHEKGMIHRDLKPVN
                                                                                                                                                                                                                                  854 IFLDS-DDHVKIGDFGLATDHLAFSADSKQDDQTGDLIKSDPSGHLTGMVGTALYVSPE-
                                                                                                                                                                                                                                                    Haem-regulated eukaryotic initiation factor 2 alpha kinase; differentiation; cell division; protein synthesis; cancer; cell proliferation; chronic myelogenous leukaemia; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding the haem-regulated eukaryotic initiation factor alpha kinase - used as an anti-viral and anti-proliferative agent, esp. against cancer and psoriasis
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                                                                                                   580 QRQFSRYFIEFEELQLLGKGAFGAVIKVQNKLDGCCYAVKRIPINPASR-QFRRIKGEVT 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      880 kvylyiqmqlcrkenlkdwmngrctiee---rersvclhiflqiaeaveflhskglmhrd 936
                                                                                    908 VSPE-VQGSTKSAYNQKVDLFSLGIIFFEMSYHPMVTASERIFVLNQLRDPTSPKFPEDF 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69; Gaps
                             LKPVNIFLDSDDHVKIGDFGLATDHLAFSADSKQDDQTGDLIKSDPS-GHLTGMVGTALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The eIF-2alpha kinase can be used to inhibit protein synthesis, induce cell differentiation and to prevent esp.viral infection. Skinase is also called the haem-regulated initator protein (HRI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA coding for eucaryotic cell initiation factor 2-alpha kinase used for regulation of cell proliferation and differentiation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.6%; Score 473.5; DB 14; Length 626; 32.2%; Pred. No. 3.6e-30; Live 69; Mismatches 170; Indels 69;
                                                                                                                                                                                                                                                                                                                                                                eukaryotic initiation factor 2 alpha kinase; HRI;
haem-regulated initiator; translation; protein synthesis;
rabbit reticulocyte lysate.
                                                                                                                                                               1043 tq-kypceyvmvqdmlspspmerpeainilen 1073
                                                                                                                                            967 DDGEHAKQKSVISWLLNHDPAKRPTATELLKS 998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MASI ) MASSACHUSETTS INST TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                AAR44008 standard; Protein; 626 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 2-3; 20pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for treating cancer and psoriasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= P-52
506..525
/label= P-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166..178
/label= P-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92JP-0081664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92JP-0081664
                                                                                                                                                                                                                                                                                                         12-MAY-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 146; Conservative
                                                                                                                                                                                                                                                                                                                                    Rabbit eIF-2 alpha kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  454..467
                                                                                                                                                                                                                                                                                                                                                                                                                           Oryctolagus cuniculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1993-356453/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ51296.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JP05260981-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-OCT-1993.
                                                                                                                                                                                                                                                                             . AAR44008;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
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                                                                                                                                                                                                                                                                                                                                                                : | ||| ||||| :|||| :||| || |||||| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    337 qllfghnsdve----edftsaeesseedlsalr-----htevgyhlmlhigmglc 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunosuppressive; cardiant; renal; antinflammatory; antiasthmatic; dermatological; antidiabetic; antiinfertility; gene therapy; vaccine; immune disorder; cardiovascular disease; neurodegenerative disease; cancer; autoimmune disorder; stroke; inflammatory bowel disease; inflammatory pelvic disease; multiple sclerosis; psoriasis.
                                                                                                                                                                                                                                                                                                                        580 QRQFSRYFIEFEELQLLGKGAFGAVIKVQNKLDGCCYAVKRIPINPASR-QFRRIKGEVT 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLSRLHHENIVRYYNAWIER-HERPAGPGTP--PPDSGPLA--KDDRAARGQPASDTDGL 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      383 elslwdwiaernrrsrecvdesacpyvmvsvatkifqelvegvfyihnmgivhrdlkprn 442
                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           694 DSVEAAAPPPILSSSVEWSTSGERSASARFPA-----TGPGSSDDEDDDEDEHGGVFSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SFLPASDSESDIIFDNEDENSKSQNQDEDCNEKNGCHESEPSVTTEAVHY -- LYIQMEYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             912 VQGSTKSAYNQKVDLFSLGIIFFEMSYHPMVTASERIFVLNQLR-----DPTSPKFPEDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     854 IFLDS-DDHVKIGDFGLATDHLAFSADSKQDDQTGDLIKSDPSGHLTGMVGTALYVSPE-
                                                                                                                                                                                                                                                               :69
                                                                                                                                                                                                   Length 626;
and differentiation, especially of cells with uncontrolled proliferation or arrested differentiation.
                                                                                                                                                                                                                                                            69; Mismatches 170; Indels
                                                                                                                                                                                                DB 15;
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                                                                                                                                                                                                                                 .6e-30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB65664 standard; Protein; 630 AA
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                                                                                                                                                                                                                           Best_Local Similarity 32.2*
Matches 146; Conservative
                                                                                                626 AA
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                                                                                                   Sequence
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the present suggence is a mover process. The process of and the nucleic acids that encode them may be used in the treatment and diagnosis of diseases associated with inappropriate kinase expression such as immune related diseases and disorders, cardiovascular disease, neurodegemerative diseases and/or cancers. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays. The kinase polypeptides may be used as antigens in the production of antibodies of kinase expression and activity. Anti-kinase antibodies and kinase expression and activity also be used to down regulate kinase expression and activity. Diseases related to kinase expression and activity include rheumatoid arthritis, atherosclerosis, autoimmune disorders, complications of organ transplantation, myocardial infarction, immune disorders, cardiomyopathies, strokes, renal failure, contactive stress related disorders, chronic inflammatory pelvic disease, multiple sclerosis, asthma, contactivity, diabbetes, cancers and contactivity.
                                                                                                                                                                                                                                   present sequence is a novel protein kinase. The novel protein kinases
                                                                                           Nucleic acids encoding kinase polypeptides, useful for diagnosing and treating immune-related diseases and disorders, cardiovascular disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----SDTDGLDSVEAAPPPILSSSV-E 710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   610 KLDGCCYAVKRIPINPASRQF-RRIKGEVTLLSRLHHENIVRYYNAWIERHERPAGPGTP 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            711 WSTSGERSASARFPA--TGPGSSDDEDDDEDEHGGVFSQSFLPASDSESDIIFDNEDENS 768
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519 vllel-fqpfgtemeraevltglr---tgqlpeslrk-rcpvqakyiqhltrnssqrps 573
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5.5%; Score 471.5; DB 22; Length 32.9%; Pred. No. 5.3e-30; tive 70; Mismatches 185; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22;
                                                                                                                                          neurodegenerative diseases and/or cancers -
                                                                                                                                                                                       Claim 10; Fig 1; 310pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              669 PPDSGPLAKDDRAARGQPA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reproductive disorders.
                   2001-032161/04.
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                                            N-PSDB; AAF44692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An example
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                                                                                                                                                                                                                                                                                                                                                                                                                  Screening method for identifying anti-tumour agents - based on an increase in the activity of a double stranded RNA-activated protein
                                                                                                             Human; PKR; double stranded RNA-activated protein kinase; neoplasm; cell growth; differentiation; tumour suppressor; tumourigenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.9%; Score 415.5; DB 18; Length 550;
25.7%; Pred. No. 1.9e-25;
tive 69; Mismatches 166; Indels 217;
                                                                                                                                                                                                                                                                                                                                                    Sonenberg N;
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                                                                                                                                                                                                                                                                                                                                                     Katze MG, Koromilas AE,
        AAW36139 standard; Protein; 550 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig 5; 41pp; English.
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92US-0953681.
93US-0141244.
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Matches 156; Conservative
                                                               (first entry)
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                                                                                        Human PKR protein.
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22-OCT-1993;
                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                   US5670330-A.
                                                              30-MAR-1998
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New transgenic plants resistant to viral infection contg. 2-5A-dependent RNase - useful in developing products useful in gene therapy against viral disease and cancer.
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263 gmdfkeieligsggfggyfkakhridgktyvikrvkynn-----ekaerevkalakldhv 317
                                                                                                                                                                                                                                                                                                 ----pj6p-----
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408 QLLSGLDYLHSNSVVHKVLSASNVLVDAEGTVKITDYSISKRLADICKEDVFEQTRVRFS 467
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4.9%; Score 414; DB 16; Length 551;
25.7%; Pred. No. 2.5e-25;
Live 69; Mismatches 167; Indels 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          dsRNA-dependent protein kinase; PKR; 2-5A synthetase; 2-5A-dependent RNase; RNase L; 2-5A system; antiviral; RNA degradation; transgenic plant; tobacco; disease resistance; crop protection; tobacco mosaic virus; tobacco etch virus; alfalfa mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human dsRNA-dependent protein kinase.
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               Best Local Similarity 25.78
Matches 156; Conservative
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WO9639806-A1.

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antivizal protein that is believed to phosphorylate the alpha subunit of translation factor eIF2-alpha, which indirectly inhibits protein synthesis initiation. Its amino acid sequence was deduced from a PKR cDNA clone (AATT5050). Novel transgenic plants, such as synthetase (see also AAW12701) and human or mouse 2-5A-dependent RNase (see also AAW12701) and human or mouse 2-5A-dependent mosaic virus, tobacco etch virus and alfalfa mosaic virus, necrotic local lesions occur instead of typical systemic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 qlaaklaylq-----q 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.9%; Score 413; DB 18; Length 551;
25.7%; Pred. No. 3e-25;
tive 69; Mismatches 167; Indels 216; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           328 WSPQQLLKHSFINPQPKMPLVEQSPEDSGGQDYVETVIPSNRLPSAAFFSETQRQFSRYF 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                222 lnsssllmnglrnngrkak-----rslaprfdlpd---mketkytvdkrf 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      588 -IEFEELQLLGKGAFGAVIKVQNKLDGCCYAVKRIPINPASRQFRRIKGEVTLLSRLHHE 646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              647 NIVRYYNAWIERHERPAGPGTPPPDSGPLAKDDRAARGQPASDTDGLDSVEAAAPPPILS 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         408 QLLSGLDYLHSNSVVHKVLSASNVLVDAEGTVKITDYSISKRLADICKEDVFEQTRVRFS 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   468 DNALPYKTGKKGDVWRLGLLLLSLSQGQECGEYPVTIPSDLPADFQDFLKKCVCLDDKER 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----- dgfd----- 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         707 SSVEWSTSGERSASARFPATGPGSSDDEDDDEDEHGGVFSQSFLPASDSESDIIFDNEDE 766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           767 NSKSQNQDEDCNEKNGCHESEPSVTTEAVHYLYIQMEYCEKSTLRDTID--QGLYRDTVR 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 885 QTGDLIKSDPSGHLTGMVGTALYVSPEVQGSTKSAYNQKVDLFSLGIIFFEMSYHPMVTA 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    825 LWRLFREILDGLAYIHEKGMIHRDLKPVNIFLDSDDHVKIGDFGLATDHLAFSADSKQDD 884
                                                                                                                                                                                                                                                                 synthetase - have increased resistance to viral infection esp. to tobacco mosaic virus, tobacco etch virus or alfalfa mosaic virus
                                                                                                                                                                                                                                                 Transgenic plants co-expressing 2-5A-dependent RNase and 2-5A
                                                                                                                                                                                                                                                                                                                                                             Human dsRNA-dependent protein kinase (PKR) (AAW12705) is an
                                                                                                                                                                                                                                                                                                                           Disclosure; Page 146-148; 189pp; English.
                                                                                                              (CLEV-) CLEVELAND CLINIC FOUND.
                                        96WO-US09895.
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                                                                                                                                                  Mitra A, Silverman RH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    319 nivhyngcw-----
                                                                                                                                                                                      WPI; 1997-051617/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          551 AA;
                                                                                                                                                                                                          N-PSDB; AAT59650.
                                  07-JUN-1996;
                                                                          07-JUN-1995;
19-DEC-1996
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509 AA;

Seguence

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especially myositis, polymyositis or dermatomyositis. The recombinant protein is more sensitive to autoantibodies than HRS purified from calves' liver or HeLa cells and has better storage stability, especially being stable for more than 24 hr at -80 to 25 deg. C.
945 SERIFVLNQLRDPTSPKFPEDFDDGEHAKQKSVISWLLNHDPAKRPTATELLKSELLPPP 1004
                             489 fetskfftdlrdgi---isdifd----kkektligkllskkpedrpntseilrtltvwkk 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW25223 represents human histidyl tRNA synthetase (HRS). This sequence was produced from a human HRS gene suitable for the sepressing HRS in insect host cells, particularly Sf9 cells. The protein, or peptide fragments produced can be used in immunoassays for detecting autoantibodies associated with autoimmune diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tRNA; transfer RNA; UTR; untranslated region; primer; probe; amplification; hybridisation; detection; diagnosis; immunoassay; autoantibody; autoimmune disease; myositis; polymyositis; dermatomyositis; recombinant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant histidyl tRNA synthetase produced in insect cells -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful in immunoassays for diagnosis of autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   represents the site of a conserved substitution"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "given in the specification as "*"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "signature region 2" 378..405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "signature region 1"
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(USSH ) US NAT INST OF HEALTH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                     AAW25223 standard; Protein; 509 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Motif 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "Motif 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leff R, Nichols R, Plotz P,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human histidyl-tRNA synthetase.
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                                                                                                 1005 QMEESELH 1012
                                                                                                                                                              542 speknerh 549
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                                                                                                                                                                                                                                                                                                     1226 ILYDAVTEKLTRREVEAKFCNLSLSSNSLCRLYKFIEQKGDLQDLMPTINSLIKQ---- 1280
                                                                                                                                                                                                                                                                                                                                                                1281 KTGIAQLVKYGLKDLEEVVGLLKKLGIKLQVLINLGLVYKVQQHNGIIFQFVAFIKRQR 1340
                                                          1007 BESELHEVLHHTLTNVDGKAYRTMMAQIFSQRISPAI-----DYTYDSDILK---- 1053
                                                                                                                     1054 GNFSIRTAKMQQHVCETIIRIFKRHGAVQLCTPLLLPRNRQIYEHNEAALFM----DHSG 1109
                                                                                                                                                                                1110 MLVMLPFDLRIPFARYVARNNILNLKRYCIERVFRPRK··LDRFHPKELLECAFDIVTST 1167
                                                                                                                                                                                                                                         1168 TNSFLPTAEIIYTIYEIIQEFPALQERNYSIYLNHTMLLKAILLHCGIPEDKLSQV--YI 1225
                                                                                                                                                                                                                                                                                                                                                                                                                                           288 klsqnkqaleglgdlkllfeyltlfglddkisfdlslargldyytgvlyeavllqtpaqa 347
                                                                                                                                                                                                                                                            Query Match
4.7%; Score 399; DB 18; Length 509;
Best Local Similarity 24.7%; Pred. No. 3.8e-24;
Matches 129; Conservative 110; Mismatches 225; Indels 58; Gaps
                                                                                                                                      239 dkldkvsweevknemvge---kglapevadrigdyvqqhggv-----slveqllqdp 287
                                                                                       3 eraaleelvklqgervrglkqqkasaelieeevakllklkaqlgpdeskqkfvlktpkgt 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corn histidyl-tRNA synthetase; aminoacyl-tRNA synthetase;
AARS; herbicide; plant toxin; protein synthesis inhibition; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1453 LVSDKE--GSHVKVKSFEKERQTEKRVLETELVDHVLQKLRT 1492
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New polynucleotide encoding plant aminoacyl-tRNA synthase and the encoded polypeptide, useful e.g. for regulating gene expression -

Claim 31; Page 57-8; 74pp; English.

penzyme is an aminoacyl-tRNA synthetase (AARS). AARSs charge (acylate) specific tRNAs with amino acids for use in protein synthesis. Histidyl-tRNA synthetase therefore charges a histidyl-tRNA synthetase therefore charges a histidyl-tRNA with histidine. Since this enzyme has a crucial role in protein synthesis and likely to be toxic. The present sequence could therefore be used as a basis for testing whether the encoded aminoacyl-tRNA synthetase is sensitive to known inhibitors or other chemicals and hence could be used as a sensitive to known inhibitors or other chemicals and hence could be used in the discovery of potential herbicides. The present sequence is the corn histidyl-tRNA synthetase corn. This 495 AA; 

Sequence

1051 ILKG--NFSIRTAKMQQHVCETIIRIFKRHGAVQLCTPLLLFRNRQIYEHNBAALFM--- 1105 1106 -DHSGMLVMLPFDLRIPFARYVARNNILNLKRYCIERVFRPRKLDRFHPKELLECAFDIV 1164 1165 TSTINSFLPTAEIIYTIYEIIQEFPALQERNYSIYLNHTMLLKAILLHCGIPEDKLSQV- 1223 1282 ---TGIAQLVKYG-----LKDLEEVVGLEKKLGIKLQVLINLGLVYKVQQHNG 1326 1224 -YIILYDAVTEKLTRREVEAKFCNLSLSSNSLCRLYKFIEQKGDLQDLMPTINSLIKQK- 1281 Gaps 1327 IIFQFVAFIKRRQRAVPEILAAGGRYDLLIPQFRGPQALGPVPTAIGVSIAIDKISAAVL 1386 1387 NME----ESVTISSCDLLVVSVGQMSMSRAINLTQKLWTAGITAEIMYDWSQSQEELQEY 1442 237 ssidkldkqtfeqvkkel--------vaekgisnetadeignlyktrg 276 277 pplevlmelrkegskfmnnvgsvaalneleilfkaldkanaiskitfdlslargldyytg 336 337 viyeavf----kgaaqvgsiaaggrydnlvgmfsgkq----ip-avgvslgiervfalme 387 64; Query Match
4.4%; Score 375; DB 21; Length 495;
Best Local Similarity 27.1%; Pred. No. 3.5e-22;
Matches 127; Conservative 80; Mismatches 197; Indels 6; 1443 CRHHEITYVALVSDKEGSHVKVKSFEKERQTEKRVLETELVDHVLQKL 1490 δ δ qq QQ οy ò g

Search completed: October 22, 2001, 01:17:35 Job time: 7236 sec

445 algssipwmvlvgeselgkgtvklkdveangeeevdrkdfvrelkkrl 492